## Claims

1. (Currently amended) A method, ~~for classifying an unknown bioactive condition,~~ comprising:

generating a ~~scenario~~ scenario-to-be-classified by exposing a first biological system to two or more bioactive conditions, including [[the]] an unknown bioactive condition;

representing a response of the first biological system, or portion thereof, to the bioactive conditions~~, where representing the response of the system comprises determining data sufficient to generate~~ by generating a feature space vector;

using a database, the database comprising scenarios where each scenario was generated by exposing a second biological system to one or more bioactive conditions, the scenario being represented as feature space vector data;

determining software expert parameters, where the expert encodes a function that maps a feature space vector to a scenario;

weighting the expert parameters;

~~attempting to classify~~ classifying a scenario by database comparison using the software expert; and

outputting a classification result to a user.

2. (Original) The method according to claim 1 where the system comprises living cells.

Claims 3-8 (Canceled).

9. (Currently amended) The method according to claim [[7]] 1 where transforming the data comprises:

determining expert parameters based on extracted data, where experts encode functions that map the feature space vector to a set of scenarios; and

tuning the integrated expert.

10. (Previously presented) The method according to claim 9 where tuning the integrated expert comprises adaptive expert calibration.

Claim 11 (Canceled).

12. (Original) The method according to claim 1 where attempting to classify the bioactive condition by database comparison comprises:

exposing the system to one or more scenarios to provide sufficient data to generate a characteristic signature for the bioactive condition;

extracting data;

calculating a location of data clusters in feature space representing the characteristic signature of the bioactive condition;

comparing location of data clusters in feature space representing the characteristic signature of the bioactive condition relative to data clusters representing known bioactive conditions; and

determining a likelihood that a bioactive condition is a known bioactive condition.

13. (Previously presented) The method according to claim 12 where calculating a relative location of data clusters is done with software experts, where experts encode functions that map the feature space vector to a set of scenarios.

14. (Original) The method according to claim 1 where attempting to classify the bioactive condition comprises:

exposing the system to one or more scenarios to provide sufficient data to generate a characteristic signature for the bioactive condition;

calculating a location of data clusters in feature space representing the characteristic signature of the bioactive condition;

comparing the location of data clusters representing the characteristic signature of the bioactive condition relative to data clusters representing known bioactive conditions; and

determining a likelihood that an unknown bioactive condition is a known bioactive condition.

15. (Previously presented) The method according to claim 14 where calculating a relative location of data clusters is done with software experts, where experts encode functions that map the

feature space vector to a set of scenarios.

16. (Currently amended) The method according to claim 1 where ~~attempting to classify~~ classifying a ~~complex~~ scenario comprises:

~~synthesizing a complex scenario from~~ mathematically transforming known scenarios present in the database~~, where exposing two or more biological systems serially to two or more bioactive conditions generates~~ to generate [[the]] a complex scenario ~~following mathematical transformation~~;

comparing the ~~scenario~~ scenario-to-be-classified ~~generated by the bioactive condition~~ to the complex scenario; and

determining a likelihood that [[a]] the complex scenario is the ~~scenario~~ scenario-to-be-classified.

17. (Previously presented) The method according to claim 16 where the known scenarios are simplex scenarios that are generated by exposing a single biological system serially to two or more bioactive conditions.

18. (Previously presented) The method according to claim 17 where each simplex scenario is generated by applying an elicitor, where the elicitor comprises bioactive conditions and a protocol used to apply the bioactive conditions to one or more biological systems.

Claim 19 (Canceled).

20. (Previously presented) The method according to claim 18 where the elicitor has known effects on the system.

21. (Previously presented) The method according to claim 18 where the elicitor has unknown effects on the system.

22. (Original) The method according to claim 18 comprising repeatedly applying an unknown bioactive agent in combination with one or more elicitors.

Claims 23-79 (Canceled).

80. (Original) The method according to claim 1 useful for classifying unknown drug candidates.

81. (Original) The method according to claim 1 useful for classifying unknown toxins.

82. (Original) The method according to claim 81, comprising:

identifying cell type and cell response most useful for providing information concerning cellular response to a particular scenario;

generating a database of scenarios; and

classifying unknowns by comparison with numerical feature space vector created by known scenarios.

83. (Original) The method according to claim 1 the system comprises non-pigmented cells.

Claims 84-107 (Canceled).

108. (Original) A computer program encoding the method of claim 1.

109. (Original) A computer programmed with the computer program of claim 108.

110. (Original) A computer-readable medium on which is stored a computer program having instructions for executing the method of claim 1.

Claims 111-114 (Canceled).

115. (Original) The method according to claim 2 where the change detected in the living cells is cytoplasmic streaming.